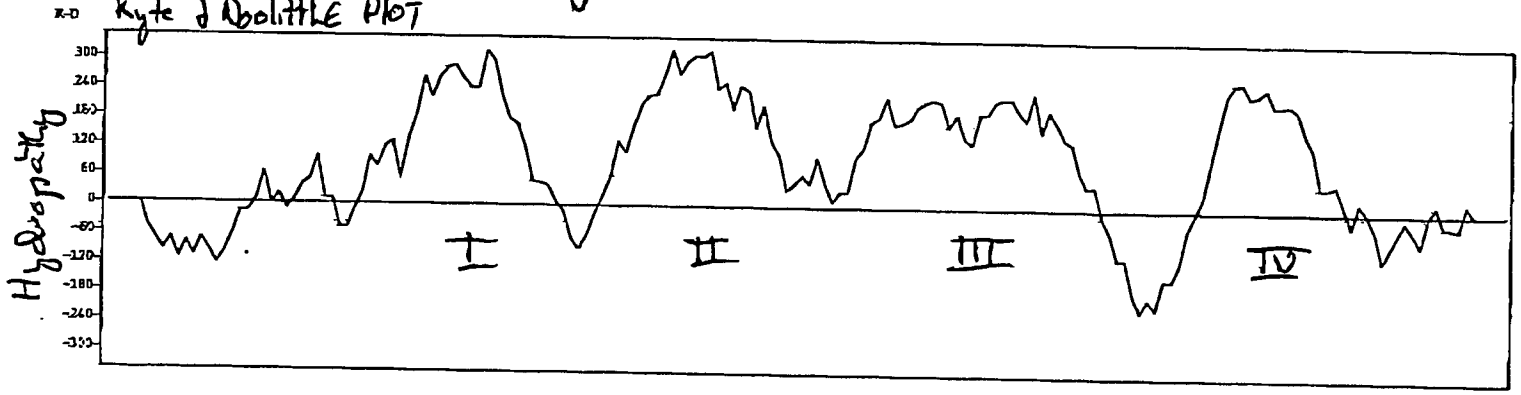
Trans of plasmolipin Seque[illegible]

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
MAEFPSKVST	RTSSPAQGAE	ASVSALRPDL	GFVRSRLGAL	MLLGLVLGLL	50
VWALIADTPY	HLYPAYGWVM	FVAVFLWLVT	IVLFNLYLFQ	LHMRLYMVPW	100
PLVLMIFNIS	AIVLYTTAFI	ACSAAVDLTS	LRGIRPYNQR	AAASFFACLV	150
MIAYGVSAFF	SYQAWRGVGS	NAATSQMAGG	YA		182

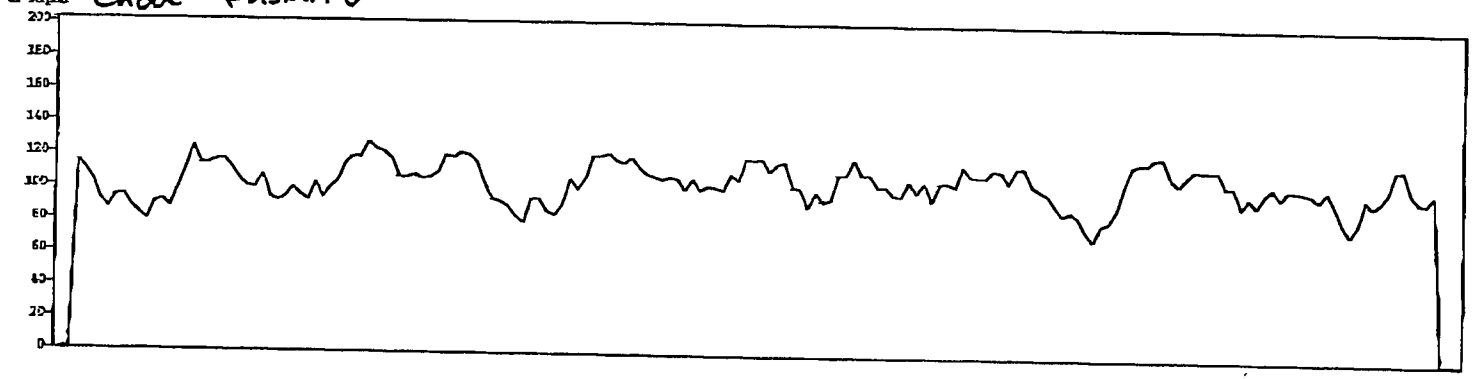
GeneDocks 2.4 version 1994

Hydrophobic Region I-IV

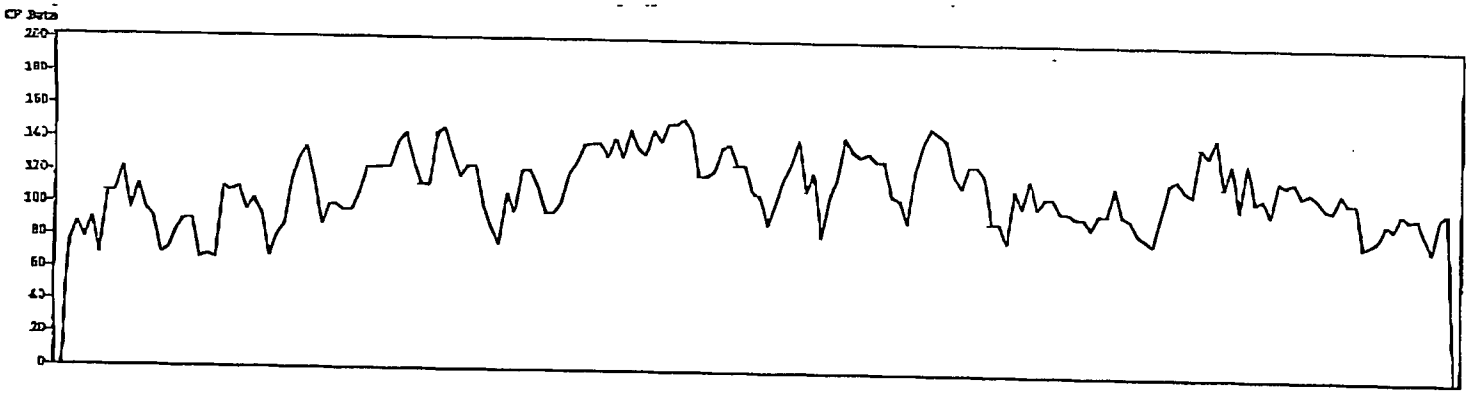
Kyte & Doolittle PLOT



Chou-Fasman



high α helical content when Alpha > 103 (Ave) & Alpha > B[illegible]



10/18/2

10/18/2002 FRI 11:47 [TX/RX NO 6300] 003
OCT.18.2002 12:23PM STEVE CHIKEN NO.139 P.3/1

Help on Kyte-Doolittle Hydrophobicity

Kyte-Doolittle Hydrophobicity predicts regions of hydrophobicity by summing the hydrophobicity values for each amino acid over a specified range of amino acids.

Kyte and Doolittle recommend a range between 7 and 13. The default in GeneWorks is 11 (5 before and 5 after a given residue). The values are then multiplied by 10 to make them integers. The results appear in the column with the default name "K-D".

Reference: Kyte, J., and Doolittle, R.F. 1982. *Journal of Molecular Biology* 157: 105-132.

The parameter settings for this algorithm can be changed in the **Edit Parameters dialog box**, which is accessible using the **Params button**.

In the **Edit Parameters dialog box:**

Column Label shows the name of the algorithm selected. This name will also appear as the column header in the **Analysis Table view**. You can change the name to make it easier to identify the contents of the column. The default column name is "K-D".

N- range and **C-Range** are text boxes that determine the size of the window around a base. Kyte and Doolittle recommend a range between 7 and 13. The default in GeneWorks is 11 (5 before and 5 after a given residue).

The **Additive Factor** is a factor that is added to the value; the default is 0. The **Mult(iplicative) Factor** is a factor by which the value is multiplied; the default is 1.

Note: The default settings for each algorithm are those recommended in the original papers. These settings were chosen because they provide the best balance between sensitivity and noise reduction. If you choose other settings, you must be aware that your results will differ from those of the authors.

Idle Priority allows you to determine how quickly the calculations for the column will be carried out. All of the calculations are run in the background (e.g., you can perform other tasks while they are being done) unless you choose **Immediate** for the **Idle Priority**. Then the calculations are done in the foreground (e.g., you will have to wait until the calculation finishes in order to perform other tasks). **Off** stops the calculation of the values in the column.

Help on Chou-Fasman Indices

Chou-Fasman Indices predict the location of alpha helices, beta sheets, and beta turns in a protein using average values of the conformational potentials Pa, Pb, and Pt from Tables V and VII of Chou and Fasman (1978).

The "CF Alpha" score is the average over a specified range of the sequence. The default range is from 2 residues before to 3 residues after a given residue. If the average Pa is greater than or equal to 103 and the average Pa is greater than the average Pb, that amino acid is considered to be part of an alpha helix. Values are multiplied by 100 to make them integers.

The "CF Beta" score is the average over a specified range of the sequence. The default range is 3 residues centered on a given residue. If "CF Beta" is greater than or equal to 105 and the average Pb is greater than the average Pa, that amino acid is considered to be part of a beta sheet. Values are multiplied by 100 to make them integers.

"CF Turn4" is the average conformation value of the four positions of a beta turn. The default range is from 1 residue before to 2 residues after a given residue. Values are multiplied by 100 to make them integers.

"CF Turn2" is the average conformation value of the two central positions of the turn. The default range is a given residue and the one following it. Values are multiplied by 100 to make them integers.

Reference: Chou, P.Y., and Fasman, G.D. 1978. *Advances in Enzymology* 47: 45-148.

The parameter settings for this algorithm can be changed in the **Edit Parameters dialog box**, which is accessible using the **Params button**.

In the **Edit Parameters dialog box:**

Column Label shows the name of the algorithm selected. This name will also appear as the column header in the **Analysis Table view**. You can change the name to make it easier to identify the contents of the column. The default column names are "CF Alpha", "CF Beta", CF

Turn4", and "CF Turn2",.

N- range and **C-Range** are text boxes that determine the size of the window around a residue. The default range is 21 (10 before and 10 after a given residue). The default range for "CF Alpha" is from 2 residues before to 3 residues after a given residue. If the average Pa is greater than or equal to 103 and the average Pa is greater than the average Pb, that amino acid is helical. The default range for "CF Beta" is 3 residues centered on a given residue. If "CF Beta" is greater than or equal to 105 and the average Pb is greater than the average Pa, that amino acid is a beta sheet. The default range for "CF Turn4" is from 1 residue before to 2 residues after a given residue. The default range for "CF Turn2" is a given residue and the one following it.

The **Additive Factor** is a factor that is added to the value; the default is 0. The **Mult(iplicative) Factor** is a factor by which the value is multiplied; the default is 1.

Note: The default settings for each algorithm are those recommended in the original papers. These settings were chosen because they provide the best balance between sensitivity and noise reduction. If you choose other settings, you must be aware that your results will differ from those of the authors.

Idle Priority allows you to determine how quickly the calculations for the column will be carried out. All of the calculations are run in the background (e.g., you can perform other tasks while they are being done) unless you choose **Immediate** for the **Idle Priority**. Then the calculations are done in the foreground (e.g., you will have to wait until the calculation finishes in order to perform other tasks). **Off** stops the calculation of the values in the column.